

FIG. 1A

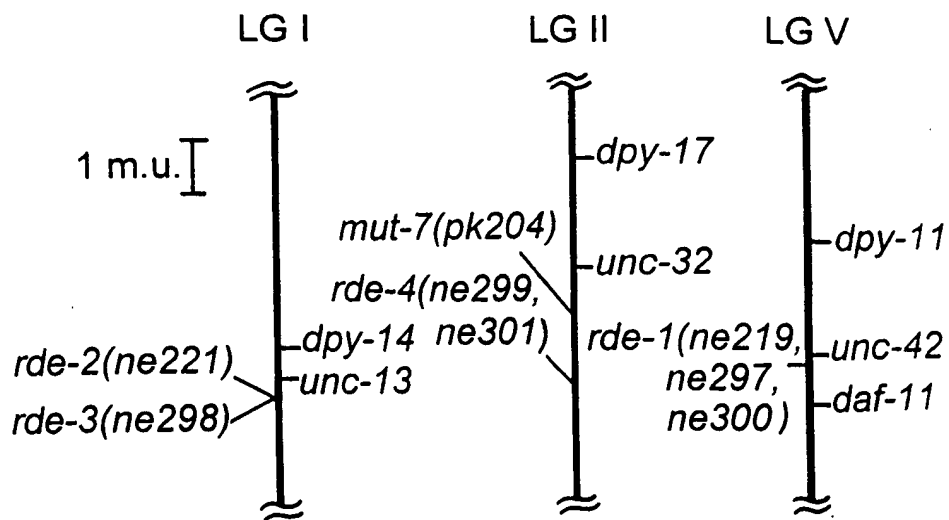
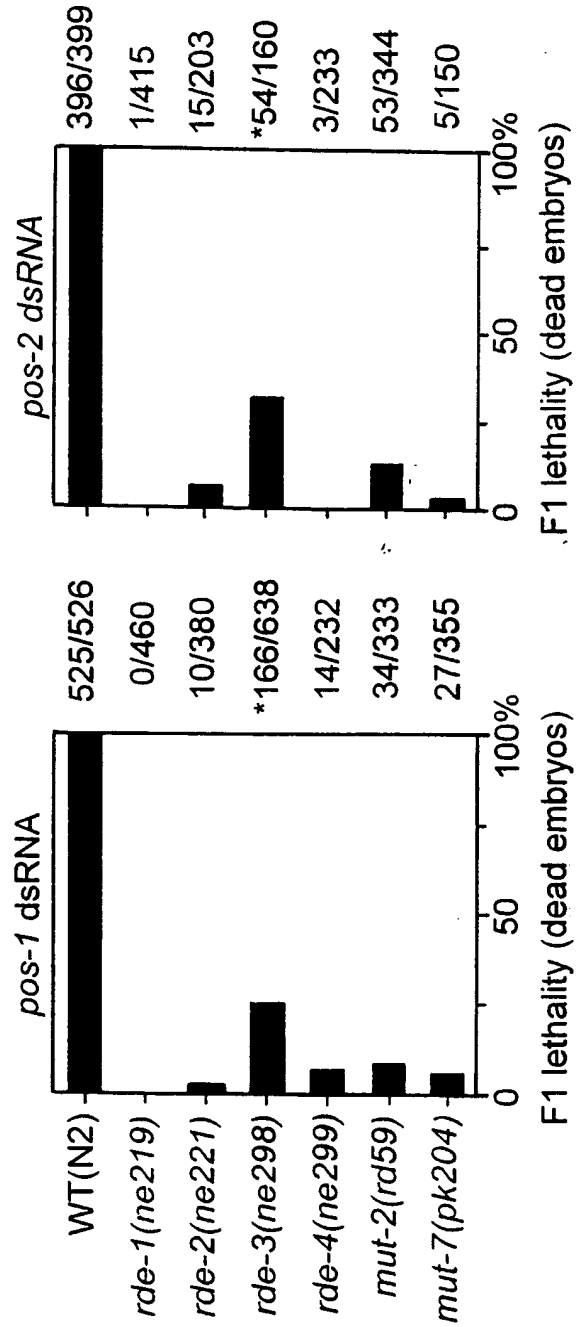
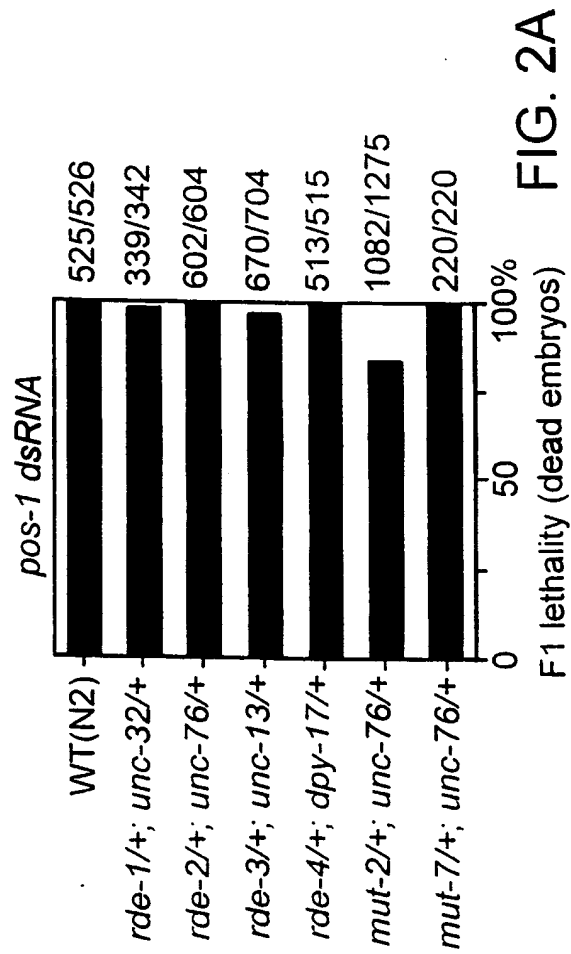


FIG. 1B



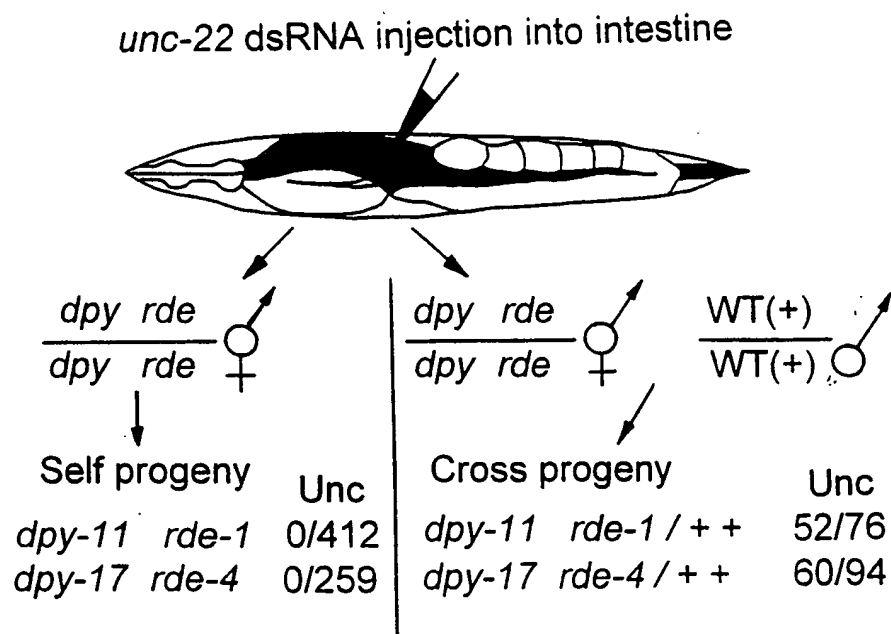
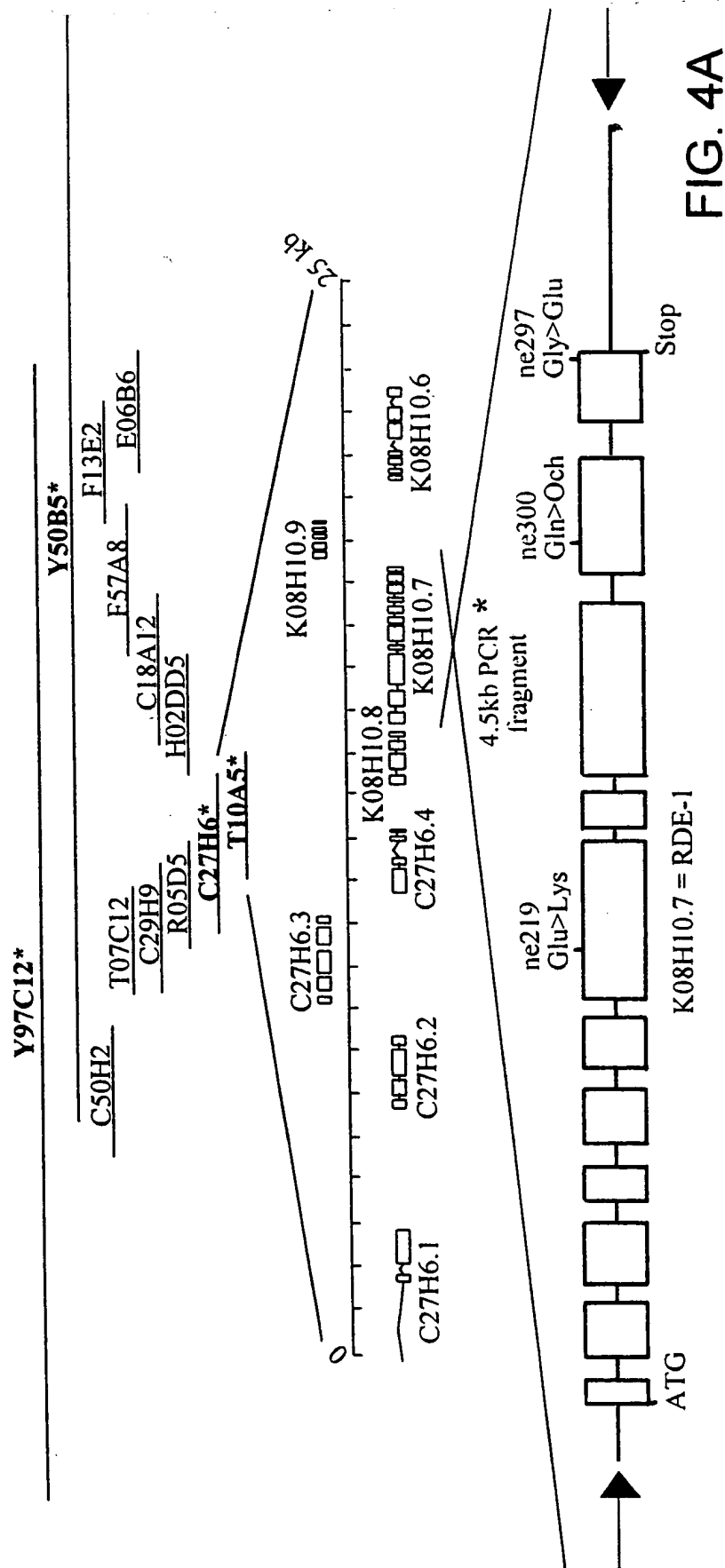


FIG. 3



Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

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RDE-1      203  VN-----EEIKVQAEAKNFVYDNNNSLRVPESFHDENRFEQSEVAPRIEAWFGVIGIGIKELEFGEPVLN-----
F48F7.1    235  S-----AVRQFSVSLRWYGVQVSLTEEDAMEGRVROVPEAVQAMDVIER-HLPSEKRYTPVGRSEFFSEVPVNASGVMAAGSCPPQASGAV
eIF2C      77  -----GKDRIFKVSIGKVSCHVSOAHEDNISGLPSVPEITIOALDVMR-HLPSMRYTPVGRSEFTASEG-----CS
ZWILLE     226  GIINGPKRERSYKVAKEVARANMHIGEFLAGKRADCEPQAVQIETIR-ESVAFECFVGRSEFSDIK-----
Sting      189  -----RAGENIEIKKAVSGVQSDAQFQVNLILRRAMEGDLKMSRYDYDQAKIN-----

RDE-1      267  -----FAIVDKFYFNAPKRGSLDYLILVDPOSQNDVVRQDKTKKLMAGKMTIRQAARPRIR-----OLLENLRLKCAE
F48F7.1    319  AGGAHSAGQYHAESKIGGGRENVHGFHQSVRPSQWKMGINIDVSAFAYRSMFVIERIAEVIELPQALAEERRALSDAQRVPTKEIRGL
eIF2C      144  -----NE--LGGGRENVHGFHQSVRPSLMQMGMINIDVSAFAYRSMFVIERIAEVIELPQALAEERRALSDAQRVPTKEIRGL
ZWILLE     297  -----TPQRLGEGLESWCGEYQSIPTQMGISINIDMASAFIEPPEVIEFVAQLIGKIVLSKPLS-----DSDAVKIKKGLRGV
Sting      244  -----LENFRMQMPGYQTSIRQHENDILICSEICHKVMETETLYNILSDAIRDSDDYQSTFK-----R-AV

RDE-1      336  VWDNEMSRITERHLTFDLCEENSLVYKVTGKSD--RGRNAKTYDTTLFKIYEENKKEFIEFPHLPLVKVKGSAKEYAVPMHEHLEVHEKPO
F48F7.1    409  KIEITHCGGOMRRKRVNVRPAQOTTFPLQL-----ETGQIECHVAKFYDKYRIQHKYPHLPCLQVGOQCKRTYLPPEVCNIVP-GQ
eIF2C      220  KVEITHCGGOMRRKRVNVRPAQOTTFPLQL-----ESQTVECTVQYFKDRHKLVRYPHLPCLQVGOQCKRTYLPPEVCNIVP-GQ
ZWILLE     372  KVEVTHRANVRKRYVAGLTPTPTRELMPVD-----EN--CTMKSVEIEYFOEMYGFTIOHLPCLQVGNQKASTPMEACKIVE-GQ
Sting      305  MGVILTDYNNKTYRIDVDVDFQSTPLCKEKTNDGEISYVDYKRYNYIIRDLPQIMSRPTDKNIRGENDQAIMIPELARATGM-TD

RDE-1      424  RYKNEIDLVMODKFLKRAKTRKPHDYKENTLKLMLKELDFSSSEELNEVERFGLCSKLQMIIECPGKVIKEPMLVNSVNEQIKMTPVIRGFOEK
F48F7.1    494  RQTKKLTBQVQSTYKATARSAPEREREISNLVRKAESAD--FEAHEFGTITNPAMTEVKGRVLSAPKLLYGGRTIR-ATALENQGWNDM
eIF2C      305  RQTKKLTBQVQSTYKATARSAPEREREISNLVRKAESAD--FEAHEFGTITNPAMTEVKGRVLSAPKLLYGGRTIR-ATALENQGWNDM
ZWILLE     454  RYTRRENEKQITALKRVTCQRAEGQRNDILRTVQHNAYDQD--PYAKEFGMNISEKIASVEARILPAPWLKHEHNGKEDCLQVQVQNNM
Sting      394  AMRADFRILRAMSEHTRLNPDRIERLRMFKRLKCKQSV--ETLKSWNIELDALIVEIPARVLPPEKILFGNQKIFVCDARADWTNEF
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FIG. 4B-1

Inventor: Craig C. Mello et al.

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

RDE-1	514	QLNVVPEKELCCAVFVWNETAGNCPLEENDVVKFYTELIGCKFRGIRGAGNENRGAQSHMYDATKNEVAFYKNCNTLNTGIGRFEIAATE
F48F7.1	581	RGKQFHTGCDPRWAJACNAQ-QOHVXENDRMFNFQLRASNDAGVPIVSNPCFCCKYAVGVEQVEPMFYFKQNSG----
eIF2C	392	RNKQFHTGCEPKWALACFP-PQRCQTEVHKSEFEEELRLSRDAGVTLQPCPCCKYAOQADSVGPMRHERKNTYAG----
ZWILLE	542	MNKKQINGMTVSRWACVNEF-----RSYQENVAEGECNEIGVGEVSGEEFNPEFVIPYISAPFDQVEKALKHVVYHTSMNKT-----
Sting	482	RTCSMFKNVHNRYVITPS-----RNLR--EIQEFVQGCIRTASSMKQNICNPIVEEIPDDRNGTSSQAIDNANAN-----
RDE-1	604	AKNMFERLPDKEQKVINFIISKRQLNAVGFVRHYQDHTIGVANQHITSETVTALASLRHEKSGKRIFYQIALKTNKLGGINQELDWS
F48F7.1	658	-----EQDAVWVLRG-KRPVYAEVVRVGDVYTGTAQCQAKNAIRHTY-----QTESNLCCKNNKLGGINSTILLPN
eIF2C	469	-----EQDAVWVLRG-KRPVYAEVVRVGDVYTGTAQCQAKNAIRHTY-----QTESNLCCKNNKLGGINSTILLPN
ZWILLE	620	-----GKELELLALLPDNNGSLYGLKICETELGLISQCLTKHVFISK-----QYLADVSEKINVMGGRNTVLVDA
Sting	552	-----DPQIYVWVVRSPNEEKYSCKIKKRTCVDREVPSSQVTLKVIAPRQQ-----KPTGLMSIATKVIQMNKLMGAP
RDE-1	694	EIAEISPEEKERRKTMPLTMYGVGIDVTHPTSYSGIDYSIAAWVASINPGGT-IYRNMIVTQEECRPGERAVAHGRE---RTDILEAKFVK
F48F7.1	725	V-----ERRIENEPTVITGCDITHPFAGDSRRKPSIAAWVSSDAHPB-RYKATVRVQOHRQETISDITY-----MVRE
eIF2C	536	G-----RPPVEQQPVITELGCDVTHPPAGDCKKPSIAAWVSSDAHPN-RYKATVRVQOHRQETISDITY-----MVRE
ZWILLE	691	IS-----CRIFLVSDIPTTILGCDVTHPENGEESSPSIAAWVASODWPEVTKYAGLICAAHROELIODHYKTWQDPVRGTVSGGMIRD
Sting	621	W-----QVVIPLHGLMTVGEDVCHSP--KNKNKSYGAETVATMDQKESFYFSTNEHIKGOELSEQMSVN-----MAC

FIG. 4B-2

* ne300

RDE-1	780	LLREFAENNDNRAPAHITWYRDGVSDSEMLRVSHDELRSKSEVKQFMSESDGEDPEPKYTFIVLOKRHNTRLLRRMEKDKPVPVVKQLTP
F48F7.1	792	LLVCEYRNTR-FKPARIWYRDGVSEGGTFNVQVELRAITREACMMTERGYQPG-----ITFTAVOKRHHTRLEAVDKDQ--V
eIF2C	603	LLIGFFKSTR-FKPTRATWYRDGVSEGGTQQVHEHLLNRENCIKLEKDYQPG-----ITFTAVOKRHHTRLECTEKNER--V
ZWILLE	775	LLISERNATG-QKPLRIHRYRDGVSEGGFYQVMELEYELDAYKACASLEPNLOPP-----VTFIVOKRHHTRLENNHNRDKNST
Sting	687	ALRSYQEQHR-SLPERITIEFRDGVGDGOLYGVNSEVNTDKDRLEIYSAGKQEGC-RMTFIIYSKRINSRYETGHRNPV-----
RDE-1	870	AETDVAAVAKQWEEDMKESKETGIVNPSGGTTVDKILVSKYKDEFEELASHHGVLGTSRPGHYTVMYDDKGMQDEYVKMTYGLAFLSAR
F48F7.1	868	-----OKAYNTPFGTTVDVGIHTPTTEDEFLCSHAGTQCTSRPSHYHVRVDDNNITATADELOQTYQMCHTYR
eIF2C	679	-----OKSGNTPAGTTVDKNTHTPTTEDEFLCSHAGTQCTSRPSHYHVRVDDNNRSSDELOITYLCHTAAR
ZWILLE	853	-----DRSGNRLGTTVDKNTCHPTTEDEFLCSHAGTQCTSRPAHYHVRVDDNNNTDGIQSTENNLCYTYAR
Sting	766	-----E-GTWVDDVITLEERYDDEFLVSOAVRIGTVPSTSNVISDNNNGENADKLOMSYKMTHTMFIN
RDE-1	960	CRKPISLPVEVHYAHLSCCKKELRYRKYEHYICDYAQPRTHEMEFFLOTNVVKYPGMSEA----- (SEQ ID NO: 13)
F48F7.1	936	CTRSVSTPPAPAYAHLYAHFRARVHLVDRHDSDGSGSOPSGHSEDITLSNNMARAVQVILAEVLVSI----- (SEQ ID NO: 9)
eIF2C	747	CTRSVSTPPAPAYAHLYAHFRARVHLVDBHDSAGSHTSGQSNGRDQALAAVAVQHODTLRTMYFA----- (SEQ ID NO: 10)
ZWILLE	921	CTRSVSTVPPAPAYAHILAAAPRPFYEEPEIMQDNQSPGKKNKTKTTVGDVGVEPLPALKENVKRVMEYC----- (SEQ ID NO: 6)
Sting	827	YSGTIRVPAVCHYAHKLAFLVAESINRAPSAGLQNLFL----- (SEQ ID NO: 7)

FIG. 4B-3

cagccacaagtgatgaacatgtctctcgaatttcccgaattggaaaaaggattttatcgtcattctctcgatccggta
tgatcaattattagcagctataagataataaagtgttgataattatattatagggagatgaaatggcttgcgagggccactg
gtaaatgcgacggcaaatctctatgagaaagaaagtactcttttggtaaatggttcaagtctccagcaaaatttacgat
cgggaatactacgagtatgaaagtgaaaatgacaaaggaaagtattgaatagaaaaaccaggaaaaacctttcccaaaaaag
agaaattccaatgtaagtgtgttaaatagtcaaaaactaattttatttttcagtcgccgatcgtgcaaaaactctctcggc
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gtttgtcgaactgaacactgtcacatcaaaaaatgctggttcggagaaagttagtaaaaaaggattcggagaaaaaagatg
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atccggaanaagacgaagacgaatcggaggttacaaattcctgaagggttatgaaaaaacacgcattatacaacaa
ttagcttcagaatgttatgacccagaaagttctctacgcgcttttgtgaacgagagattaaagtgtgagttgcaata
ataataataataatcaccicaactatttatattttaagacaattcgcgaaaaattttgtgtacgataataatcaat

FIG. 5A

tctgagagttcctgaatcgtttcacgateccaaacagattcgaacaatcattagaagtagcaccaagaatcgaagcatggt
ttggaatttacattggaatcaaagaattgttcgatggggaacctgtgctcaattttgcaagtaagttgagaaactgcga
taaaaaatcatgtgattttgttgaagttgtcgataaaactattctacaatgcaccgaaaatgtctcttctgattatett
ctcctaattgtcgacccccagtcgtgtaacgatgatgtacgaaaagatcttaaaacaaaactgatggcgggaaaaatgac
aatcagacaagccgcgcggccaagaattcgacaattattggaaaattgaagctgaaatgcgcagaagttgggataac
aaatgttagtttaaattattcaaacattaatatacaaatgtatttcaggctcgagattgacagaacgacatctgacatt
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ggagcaaaagaatacgtgtaccaatggaacatcttgaagttcatgagaagccacaaagatacaagaatcgaattgatc
ggtgatgcaagacaagtttctaaagcgagctacacgaaaacctcacgactacaaagaaaataacctaaaaatgctgaaa
aattggatttctcttctgaagagctaaattttgttgaagatttggattatgtctcaaaacttcagatgatcgaatgtcca
ggaaagggttttgaagagccaatgcttgtgaatagtgtaaatgaacaaattaaaatgacaccagtgttcgtggatttca
agaaaaacaattgaatgtgggtcccgaaaaagaactttgtgtgtgtttttgtagtcaacgaaacagcgggaaatccat
gcttagaagagaacgacgttgtgaagtgtttctacgtagattattccgaaatattttcagtaagttctacacccaact
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ttcgtgaaattgctcagagaattcgcagaagtgagttgtcttgagtatttaaaagatctctgggatttttaartttttg

FIG. 5B

taaaactttcagaacaacgacaatcgagcaccagcgcataattgtagtctatcgagacggagtttagcgattcggagatgcta
cgtgttagtcaatgatgagcttcgatctttaaaaaagcgaaagtaaaaaaatctcatgtcggaaacggggaatggagaaagatccaga
ggcgaagatacaacgttcattgttgattcagaaaagacacacatacacgattgcttcgaagaatggaaaaagataaagccagtg
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aatgttttcagaaaatgacctacggacttgcttttctctctgtctagatgtcgaaaaccccatctcgttgccttcgggttc
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ccacggactcgacacgaaaatggaaacattttctccaaactaacgtgaagtagccctggaaatgtcgttcgcataaacattttgc
aaaaagtgtcgcccggttcaatacaaattttcaattgttagatatgtgtactactttttttaagccccgggtttcaaaaatt
cattccatgactaacggttttcataaaattacttgaattt (SEQ ID NO:1)

FIG. 5C

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

CAGCCACAAAGTGATGAAAC- 5' UTR

1/1 31/11
ATG TCC TCG AAT TTT CCC GAA TTG GAA AAA GGA TTT TAT CGT CAT TCT CTC GAT CCG GAG
Met ser ser asn pro glu leu glu lys gly phe tyr arg his ser leu asp pro glu

61/21 91/31
ATG AAA TGG CTT GCG AGG CCC ACT GGT AAA TGC GAC GGC AAA TTC TAT GAG AAG AAA GTA
met lys trp leu ala arg pro thr gly lys cys asp gly lys phe tyr glu lys lys val

121/41 151/51
CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CGG GAA TAC TAC GAG
leu leu leu val asn trp phe lys phe ser ser lys ile tyr asp arg glu tyr tyr glu

181/61 211/71
TAT GAA GTG AAA ATG ACA AAG GAA GTA TTG AAT AGA AAA CCA GGA AAA CCT TTC CCA AAA
tyr glu val lys met thr lys glu val leu asn arg lys pro gly lys pro phe pro lys

241/81 271/91
AAG ACA GAA ATT CCA ATT CCC GAT CGT GCA AAA CTC TTC TGG CAA CAT CTT CGG CAT GAG
lys thr glu ile pro ile pro asp arg ala lys leu phe trp gln his leu arg his glu

301/101 331/111
AAG AAG CAG ACA GAT TTT ATT CTC GAA GAC TAT GTT TTT GAT GAA AAG GAC ACT GTT TAT
lys lys gln thr asp phe ile leu glu asp tyr val phe asp glu lys asp thr val tyr

361/121 391/131
AGT GTT TGT CGA CTG AAC ACT GTC ACA TCA AAA ATG CTG GTT TCG GAG AAA GTA GTA AAA
ser val cys arg leu asn thr val thr ser lys met leu val ser glu lys val val lys

421/141 451/151
AAG GAT TCG GAG AAA AAA GAT GAA AAG GAT TTG GAG AAA AAA ATC TTA TAC ACA ATG ATA
lys asp ser glu lys lys asp glu lys asp leu glu lys lys ile leu tyr thr met ile

481/161 511/171
CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA
leu thr tyr arg lys lys phe his leu asn phe ser arg glu asn pro glu lys asp glu

541/181 571/191
GAA GCG AAT CGG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CGC TAC GCG
glu ala asn arg ser tyr lys phe leu lys asn val met thr gln lys val arg tyr ala

601/201 631/211
CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC GCG AAA AAT TTT GTG TAC GAT AAT AAT
pro phe val asn glu glu ile lys val gln phe ala lys asn phe val tyr asp asn asn

661/221 691/231
TCA ATT CTG CGA GTT COT GAA TCG TTT CAC GAT CCA AAC AGA TTC GAA CAA TCA TTA GAA
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu gln ser leu glu

721/241 751/251

FIG. 6A

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

GTA GCA CCA AGA ATC GAA GCA TGG TTT GGA ATT TAC ATT GGA ATC AAA GAA TTG TTC GAT
val ala pro arg ile glu ala trp phe gly ile tyr ile gly ile lys glu leu phe asp

731/261 811/271
GGT GAA CCT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CCG AAA ATG
gly glu pro val leu asn phe ala ile val asp lys leu phe tyr asn ala pro lys met

841/281 871/291
TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA
ser leu leu asp tyr leu leu leu ile val asp pro gln ser cys asn asp asp val arg

901/301 931/311
AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA
lys asp leu lys thr lys leu met ala gly lys met thr ile arg gln ala ala arg pro

961/321 991/331
AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA
arg ile arg gln leu leu glu asn leu lys leu lys cys ala glu val trp asp asn glu

1021/341 1051/351
ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT
met ser arg leu thr glu arg his leu thr phe leu asp leu cys glu glu asn ser leu

1081/361 1111/371
GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA
val tyr lys val thr gly lys ser asp arg gly arg asn ala lys lys⁴ tyr asp thr thr

1141/381 1171/391
TTG TTC AAA ATC TAT GAG GAA AAC AAA AAG TTC ATT GAG TTT CCC CAC CTA CCA CTA GTC
leu phe lys ile tyr glu glu asn lys lys phe ile glu phe pro his leu pro leu val

1201/401 1231/411
AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG
lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu

1261/421 1291/431
AAG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA
lys pro gln arg tyr lys asn arg ile asp leu val met gln asp lys phe leu lys arg

1321/441 1351/451
GCT ACA CGA AAA CCT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT
ala thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp

1381/461 1411/471
TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG
phe ser ser glu glu leu asn phe val glu arg phe gly leu cys ser lys leu gln met

1441/481 1471/491
ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA
ile glu cys pro gly lys val leu lys glu pro met leu val asn ser val asn glu gln

1501/501 1531/511
ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA
ile lys met thr pro val ile arg gly phe gln glu lys gln leu asn val val pro glu

FIG. 6B

1561/521 1591/531
AAA GAA GTT TGC TGT GGT GTT TTT GTA GTC AAC GAA ACA GCG GGA AAT CCA TGC TTA GAA
lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu

1621/541 1651/551
GAG AAC GAC GTT GTT AAG TTC TAC ACC GAA CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA
glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile

1681/561 1711/571
CGA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT
arg ile gly ala asn glu asn arg gly ala gln ser ile met tyr asp ala thr lys asn

1741/581 1771/591
GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala

1901/601 1831/611
GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gln lys val leu met

1861/621 1891/631
TTC ATT ATC ATT TCC AAA CGA CAA CTG AAT GCT TAC GGT TTT GTG AAA CAT TAT TGC GAT
phe ile ile ile ser lys arg gln leu asn ala tyr gly phe val lys his tyr cys asp

1921/641 1951/651
CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA
his thr ile gly val ala asn gln his ile thr ser glu thr val thr lys ala leu ala

1981/661 2011/671
TCA CTA AGG CAC GAG AAA GGA TCA AAA CGA ATT TTC TAT CAA ATT GCA TTG AAA ATC AAC
ser leu arg his glu lys gly ser lys arg ile phe tyr gln ile ala leu lys ile asn

2041/681 2071/691
GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA
ala lys leu gly gly ile asn gln glu leu asp trp ser glu ile ala glu ile ser pro

2101/701 2131/711
GAA GAA AAA GAA AGA CCG AAA ACA ATG CCA TTA ACT ATG TAT GTT GGA ATT GAT GTA ACT
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr

2161/721 2191/731
CAT CCA ACC TCC TAC AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn

2221/741 2251/751
CCA GGT GGA ACT ATC TAT CGA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT GAG
pro gly gly thr ile tyr arg asn met ile val thr gln glu glu cys arg pro gly glu

2281/761 2311/771
CGT GCA GTG GCT CAT GGA CCG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu

2341/781 2371/791
ATC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA
leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg

FIG. 6C

2401/801	2431/811
GAC GGA GTT AGC GAT TCG GAG ATG CTA CGT	GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA
asp gly val ser asp ser glu met leu arg	val ser his asp glu leu arg ser leu lys
2461/821	2491/831
AGC GAA GTA AAA CAA TTC ATG TCG GAA CGG	GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG
ser glu val lys gln phe met ser glu arg	asp gly glu asp pro glu pro lys tyr thr
2521/841	2551/851
TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA	CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG
phe ile val ile gln lys arg his asn thr	arg leu leu arg arg met glu lys asp lys
2581/861	2611/871
CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT	GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA
pro val val asn lys asp leu thr pro ala	glu thr asp val ala val ala ala val lys
2641/881	2671/891
CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA	GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA
gln trp glu glu asp met lys glu ser lys	glu thr gly ile val asn pro ser ser gly
2701/901	2731/911
ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA	TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT
thr thr val asp lys leu ile val ser lys	tyr lys phe asp phe phe leu ala ser his
2761/921	2791/931
CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA	CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA
his gly val leu gly thr ser arg pro gly	his tyr thr val met tyr asp asp lys gly
2821/941	2851/951
ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC	TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT
met ser gln asp glu val tyr lys met thr	tyr gly leu ala phe leu ser ala arg cys
2881/961	2911/971
CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT	CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG
arg lys pro ile ser leu pro val pro val	his tyr ala his leu ser cys glu lys ala
2941/981	2971/991
AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT	TAC ATC GGT GAC TAT GCA CAG CCA CGG ACT
lys glu leu tyr arg thr tyr lys glu his	tyr ile gly asp tyr ala gln pro arg thr
3001/1001	3031/1011
CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT	AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA
arg his glu met glu his phe leu gln thr	asn val lys tyr pro gly met ser phe ala
3061/1021	3091/1031
TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA	ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT
OCH (SEQ ID NO:3)	
3121/1041	3151/1051
TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT	TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA
3191/1061	
CTT GAA ATT TAA AAA AAA AAA AAA AAA	(SEQ ID NO:2)

FIG. 6D

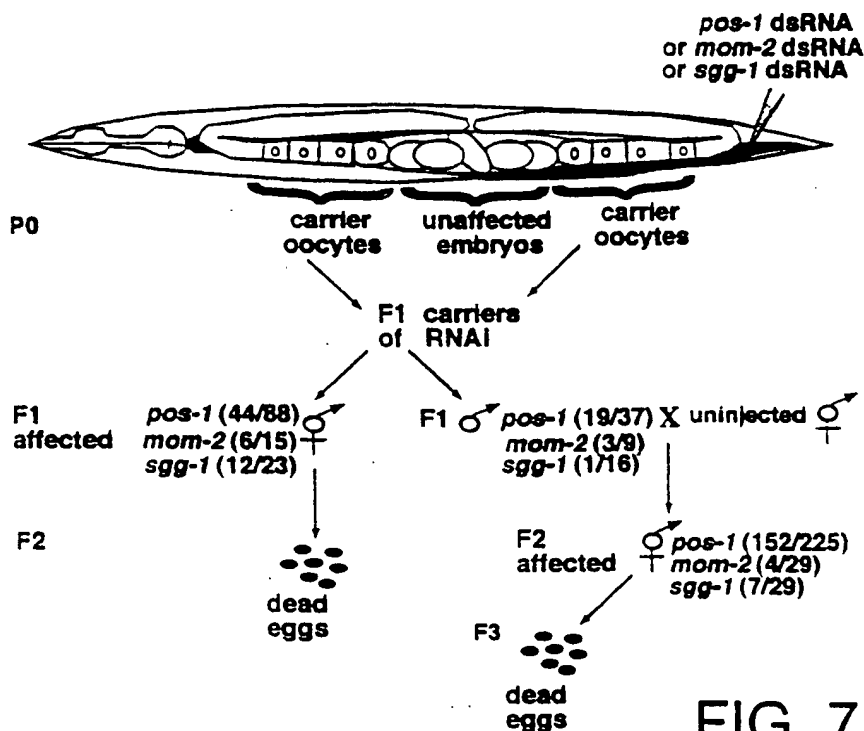


FIG. 7A

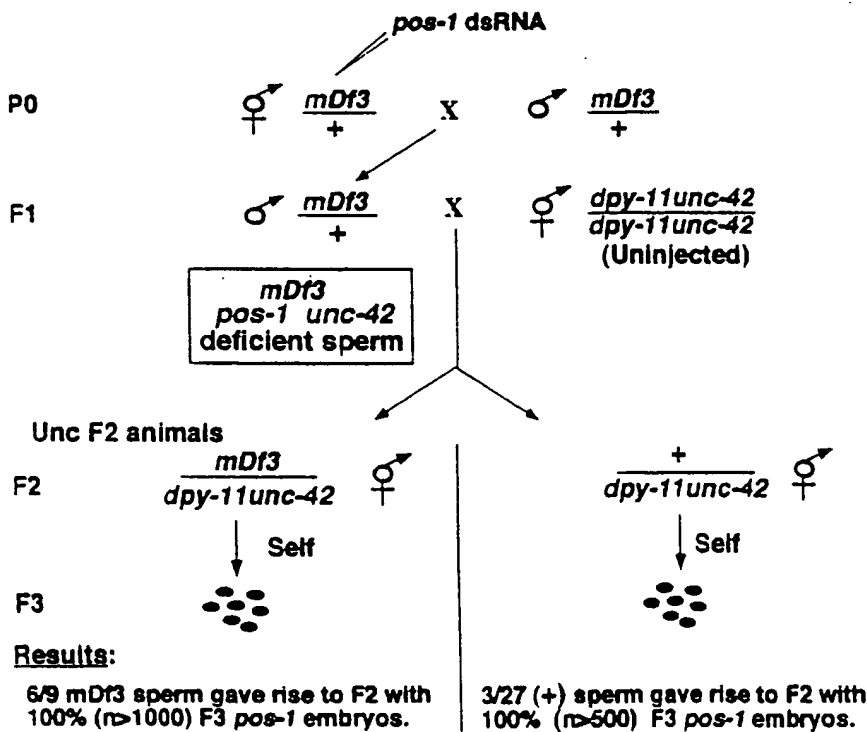


FIG. 7B

Injected P0	F1
$\frac{\text{pos-1 dsRNA}}{rde-1 \text{ unc-42}}$ $\frac{\text{♀}}{+}$	$\xrightarrow{\text{self X}}$ $rde-1 (-)$ 11/24 $rde-1 (+)$ 9/72
$\frac{\text{pos-1 dsRNA}}{rde-2 \text{ unc-13}}$ $\frac{\text{♀}}{+}$	\longrightarrow $rde-2 (-)$ 0/39 $rde-2 (+)$ 23/78
$\frac{\text{pos-1 dsRNA}}{mut-7 dpy-17}$ $\frac{\text{♂}}{+}$	\longrightarrow $mut-7 (-)$ 0/15 $mut-7 (+)$ 20/50
$\frac{\text{pos-1 dsRNA}}{rde-4 \text{ unc-69}}$ $\frac{\text{♀}}{+}$	\longrightarrow $rde-4 (-)$ 5/15 $rde-4 (+)$ 11/48

FIG. 8A

P0	Injected F1
$\frac{\text{pos-1 dsRNA}}{rde-1 \text{ unc-42}}$ $\frac{\text{♀}}{+}$	\longrightarrow $\frac{\text{pos-1 dsRNA}}{rde-1 \text{ unc-42}}$ 0/37
$\frac{\text{pos-1 dsRNA}}{rde-4 \text{ unc-69}}$ $\frac{\text{♀}}{+}$	\longrightarrow $\frac{\text{pos-1 dsRNA}}{rde-4 \text{ unc-69}}$ 0/37

FIG. 8B

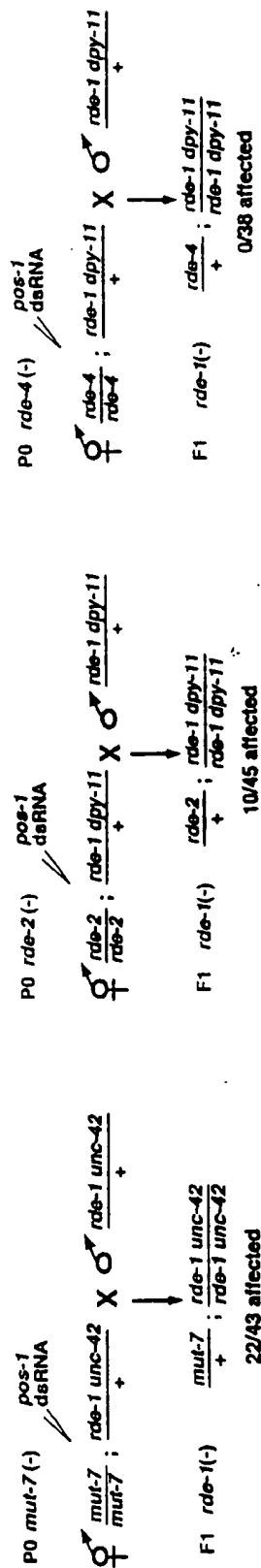


FIG. 9B

10 20 30 40 50 60
ATGGATTTAACCAAATAACGTTTGAAGCGTTTTTCGGTGGATCAGATGTTCTATGAAG
M D L T K L T F E S V F G G S D V P M K

70 80 90 100 110 120
CCTTCCCAGATCGGAGGATAACAAAACGCCAAGAAACAGAACAGATTTGGAGATGTTTCTG
P S R S E D N K T P R N R T D L E M F L

130 140 150 160 170 180
AAGAAACTCCCCTCATGGTACTAGAAGAGGCTGCTAAGGCTGTCTATCAAAAGACGCCA
K K T P L M V L E E A A K A V Y Q K T P

190 200 210 220 230 240
ACTTGGGGCACTGTCGAACCTTCTGAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT
T W G T V E L P E G F E M T L I L N E I

250 260 270 280 290 300
ACTGTAAAAGGCCAGGCAACAAGCAAGAAAGCTGCGAGACAAAAGGCTGCTGTTGAATAT
T V K G Q A T S K K A A R Q K A A V E Y

310 320 330 340 350 360
TTACGCAAGGTTGTGGAGAAAGGAAAGCACGAAATCTTTTTTCATTCTGGAACAACCAAA
L R K V V E K G K H E I F F I P G T T K

370 380 390 400 410 420
GAAGAAGCTCTTTTGAATATTGATCAAATATCGGATAAGGCTGAGGAATTGAAACGATCA
E E A L S N I D Q I S D K A E E L K R S

430 440 450 460 470 480
ACTTCAGATGCTGTTTCAGGATAACGATAACGATGATTTCGATTCTTACAAGTGCTGAATTT
T S D A V Q D N D N D D S I P T S A E F

490 500 510 520 530 540
CCACCTGGTATTTTCGCCAACCGAGAATTGGGTGCGAAAGTTGCAGGAAAAATCTCAAAAA
P P G I S P T E N W V G K L Q E K S Q K

550 560 570 580 590 600
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGAATGAGAGAACCGAGCGTTTCTTG
S K L Q A P I Y E D S K N E R T E R F L

610 620 630 640 650 660
GTTATATGCACGATGTGCAATCAAAAAACCGAGGAATCAGAAGTAAGAAGAAGGACGCA
V I C T M C N Q K T R G I R S K K K D A

670 680 690 700 710 720
AAGAATCTTGCAGCATGGTTGATGTGGAAGCGTTGGAAGACGGTATCGAATCTCTGGAA
K N L A A W L M W K A L E D G I E S L E

730 740 750 760 770 780
TCATATGATATGGTTGATGTGATTGAAAATTTGGAAGAAGCTGAACATTTACTCGAAATT
S Y D M V D V I E N L E E A E H L L E I

FIG. 10A

790 800 810 820 830 840
CAGGATCAAGCATCCAAGATTAAAGACAAGCATTCCGCACTGATTGATATACTCTCGGAC
Q D Q A S K I K D K H S A L I D I L S D

850 860 870 880 890 900
AAGAAAAGATTTTCAGACTACAGCATGGATTTCAACGTATTATCAGTGAGCACAAATGGGA
K K R F S D Y S M D F N V L S V S T M G

910 920 930 940 950 960
ATACATCAGGTGCTATTGGAAATCTCGTTCCGGCGTCTAGTTTCTCCAGACCCCGACGAT
I H Q V L L E I S F R R L V S P D P D D

970 980 990 1000 1010 1020
TTGGAAATGGGAGCAGAACACACCCAGACTGAAGAAATTATGAAGGCTACTGCCGAGAAG
L E M G A E H T Q T E E I M K A T A E K

1030 1040 1050 1060 1070 1080
GAAAAGCTACGGAAGAAGAATATGCCAGATTCCGGGCGGCTAGTGTTTGCTGGACATGGT
E K L R K K N M P D S G P L V F A G H G

1090 1100 1110 1120 1130 1140
TCATCGGCGGAAGAGGCTAAACAGTGTGCTTGTAATCGGCGATTATCCATTTCAACACC
S S A E E A K Q C A C K S A I I H F N T

1150 1160 1170 1180 1190 1200
TATGATTTTCACGGATTGAAAATATTATTGCGTATTCCTGAAAAATGAAGCGTCTGAATGA
Y D F T D * K Y Y C V F L K N E A S E *

1210 1220 1230
TTATAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:4)
L * K K K K K (SEQ ID NO:5)

FIG. 10B

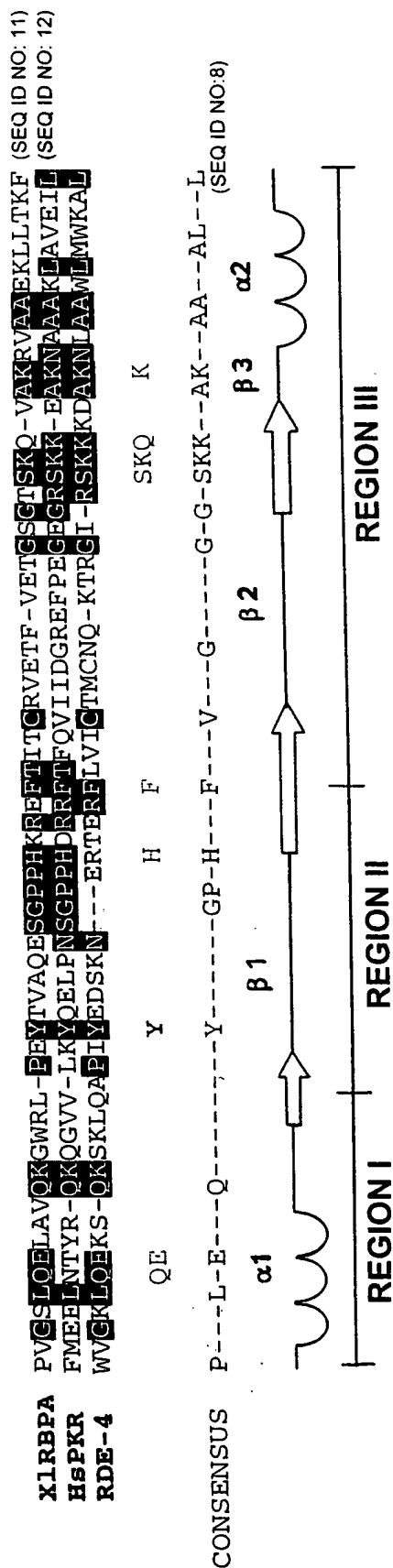
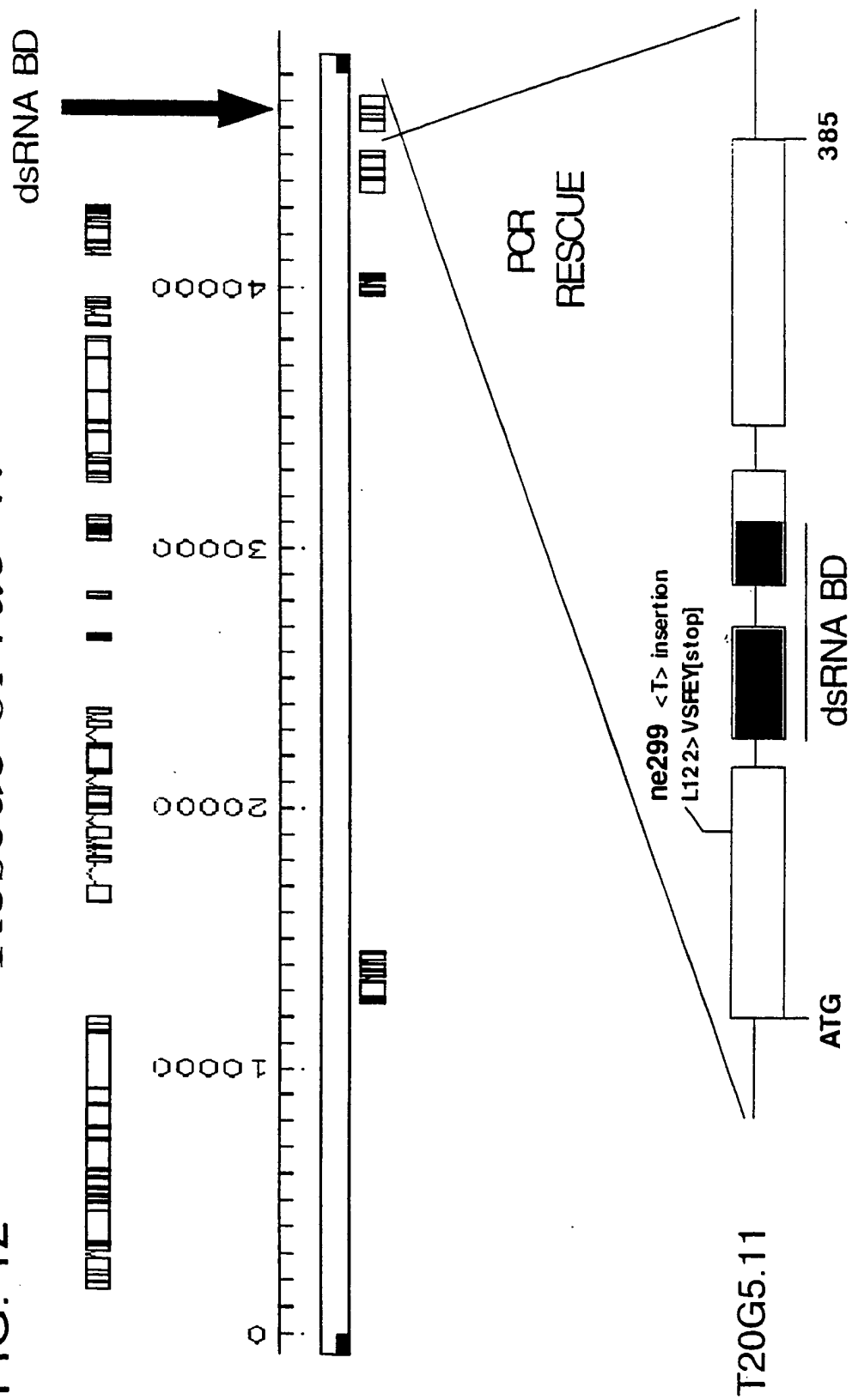


FIG. 11

Rescue of *rde-4*:

FIG. 12



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